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1600

RAW SEQUENCE LISTING

DATE: 05/06/2003

PATENT APPLICATION: US/09/652,292C

TIME: 12:01:33

Input Set : A:\EP.txt

Output Set: N:\CRF4\05062003\I652292C.raw

3 <110> APPLICANT: Bowden, Donald W.
4 Dawson, Paul A.
5 Fossey, Sallyanne C.
7 <120> TITLE OF INVENTION: GLUT10: A Novel Glucose Transporter in the Type 2 Diabetes
Linked
8 Region of Chromosome 20Q12-13.1
10 <130> FILE REFERENCE: 9151-11
12 <140> CURRENT APPLICATION NUMBER: US 09/652,292C
13 <141> CURRENT FILING DATE: 2000-08-31
15 <160> NUMBER OF SEQ ID NOS: 43
17 <170> SOFTWARE: PatentIn version 3.2
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20 <211> LENGTH: 4395
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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34 cagggcagga gggacagagg cggggcggg cgggaaagt ttgtccggcg cagcggcggtt 180
36 ggggactccg gcgggggatg cgcgcccggc ccctcagcgc ccccgacag cgcggcgagtc 240
38 ccgctcgcc atg ggc cac tcc cca cct gtc ctg cct ttg tgt gcc tct gtg 291
39 Met Gly His Ser Pro Val Leu Pro Cys Ala Ser Val
40 1 5 10
42 tct ttg ctg ggt ggc ctg acc ttt ggt tat gaa ctg gca gtc ata tca 339
43 Ser Leu Leu Gly Gly Leu Thr Phe Gly Tyr Glu Leu Ala Val Ile Ser
44 15 20 25 30
46 ggt gcc ctg ctg cca ctg cag ctt gac ttt ggg cta agc tgc ttg gag 387
47 Gly Ala Leu Leu Pro Leu Gln Leu Asp Phe Gly Leu Ser Cys Leu Glu
48 35 40 45
50 cag gag ttc ctg gtg ggc agc ctg ctg ctg ggg gct ctc ctc gcc tcc 435
51 Gln Glu Phe Leu Val Gly Ser Leu Leu Leu Gly Ala Leu Leu Ala Ser
52 50 55 60
54 ctg gtt ggt ggc ttc ctc att gac tgc tat ggc agg aag caa gcc atc 483
55 Leu Val Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile
56 65 70 75
58 ctc ggg agc aac ttg gtg ctg ctg gca ggc agc ctg acc ctg ggc ctg 531
59 Leu Gly Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu
60 80 85 90
62 gct ggt tcc ctg gcc tgg ctg gtc ctg ggc cgc gct gtg gtt ggc ttc 579
63 Ala Gly Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe
64 95 100 105 110

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68					115					120					125		
70	gtg	ggg	cca	cgg	cag	cgg	gga	gtg	ctg	gtg	tcc	ctc	tat	gag	gca	ggc	675
71	Val	Gly	Pro	Arg	Gln	Arg	Gly	Val	Leu	Val	Ser	Leu	Tyr	Glu	Ala	Gly	
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75	Ile	Thr	Val	Gly	Ile	Leu	Leu	Ser	Tyr	Ala	Leu	Asn	Tyr	Ala	Leu	Ala	
76					145					150					155		
78	ggt	acc	ccc	tgg	gga	tgg	agg	cac	atg	ttc	ggc	tgg	gcc	act	gca	cct	771
79	Gly	Thr	Pro	Trp	Gly	Trp	Arg	His	Met	Phe	Gly	Trp	Ala	Thr	Ala	Pro	
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84	175					180					185				190		
86	gag	act	gca	aca	cac	aag	gac	ctc	atc	cca	ctc	cag	gga	ggt	gag	gcc	867
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88					195					200					205		
90	ccc	aag	ctg	ggc	ccg	ggg	agg	cca	cgg	tac	tcc	ttt	ctg	gac	ctc	ttc	915
91	Pro	Lys	Leu	Gly	Pro	Gly	Arg	Pro	Arg	Tyr	Ser	Phe	Leu	Asp	Leu	Phe	
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95	Arg	Ala	Arg	Asp	Asn	Met	Arg	Gly	Arg	Thr	Thr	Val	Gly	Leu	Gly	Leu	
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98	gtg	ctc	ttc	cag	caa	cta	aca	ggg	cag	ccc	aac	gtg	ctg	tgc	tat	gcc	1011
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114	ggc	tgt	gcc	ctc	atg	gcc	ctg	tcc	gtc	agt	ggc	ata	ggc	ctc	gtc	agc	1203
115	Gly	Cys	Ala	Leu	Met	Ala	Leu	Ser	Val	Ser	Gly	Ile	Gly	Leu	Val	Ser	
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118	ttt	gcc	gtg	ccc	atg	gac	tca	ggc	cca	agc	tgt	ctg	gct	gtg	ccc	aat	1251
119	Phe	Ala	Val	Pro	Met	Asp	Ser	Gly	Pro	Ser	Cys	Leu	Ala	Val	Pro	Asn	
120					320					325					330		
122	gcc	acc	ggg	cag	aca	ggc	ctc	cct	gga	gac	tct	ggc	ctg	ctg	cag	gac	1299
123	Ala	Thr	Gly	Gln	Thr	Gly	Leu	Pro	Gly	Asp	Ser	Gly	Leu	Leu	Gln	Asp	
124	335					340					345				350		
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127	Ser	Ser	Leu	Pro	Pro	Ile	Pro	Arg	Thr	Asn	Glu	Asp	Gln	Arg	Glu	Pro	
128					355						360				365		
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138	cct	ctg	ccc	gct	cgg	ggg	cat	gca	ctg	ctg	cgc	tgg	acc	gca	ctg	ctg	1491
139	Pro	Leu	Pro	Ala	Arg	Gly	His	Ala	Leu	Leu	Arg	Trp	Thr	Ala	Leu	Leu	
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143	Cys	Leu	Met	Val	Phe	Val	Ser	Ala	Phe	Ser	Phe	Gly	Phe	Gly	Pro	Val	
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147	Thr	Trp	Leu	Val	Leu	Ser	Glu	Ile	Tyr	Pro	Val	Glu	Ile	Arg	Gly	Arg	
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254 cacacaaaaa ttaacaaaag attctgtaag aattaattgg ctatatggaa tttaggatag 4335
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262 <213> ORGANISM: Homo sapiens

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275 35 40 45
278 Phe Leu Val Gly Ser Leu Leu Leu Gly Ala Leu Leu Ala Ser Leu Val
279 50 55 60
282 Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile Leu Gly
283 65 70 75 80
286 Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu Ala Gly
287 85 90 95
290 Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe Ala Ile
291 100 105 110
294 Ser Leu Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu Val Gly
295 115 120 125
298 Pro Arg Gln Arg Gly Val Leu Val Ser Leu Tyr Glu Ala Gly Ile Thr
299 130 135 140
302 Val Gly Ile Leu Leu Ser Tyr Ala Leu Asn Tyr Ala Leu Ala Gly Thr

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311          180          185          190
314 Ala Thr His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala Pro Lys
315          195          200          205
318 Leu Gly Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe Arg Ala
319          210          215          220
322 Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu Val Leu
323 225          230          235          240
326 Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala Ser Thr
327          245          250          255
330 Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val Leu Ala
331          260          265          270
334 Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr Ala Met
335          275          280          285
338 Gly Leu Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Leu Ala Gly Cys
339          290          295          300
342 Ala Leu Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser Phe Ala
343 305          310          315          320
346 Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn Ala Thr
347          325          330          335
350 Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp Ser Ser
351          340          345          350
354 Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro Ile Leu
355          355          360          365
358 Ser Thr Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp Pro Ser
359          370          375          380
362 Ala Pro Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro Pro Leu
363 385          390          395          400
366 Pro Ala Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu Cys Leu
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371          420          425          430
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386 Leu Tyr Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr Leu Phe
387          485          490          495
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